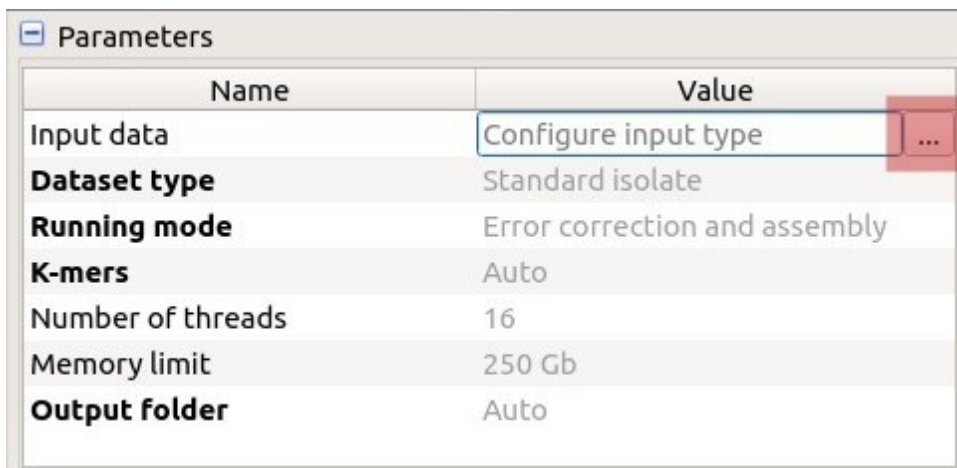


Assemble Reads with SPAdes Element

Performers assembly of input short reads.

Parameters in GUI

Parameter	Description	Defaultvalue
Input data	<p>Select the type of input for SPAdes. URL(s) to the input files of the selected type(s) should be provided to the corresponding port(s) of the workflow element.</p> <p>At least one library of the following types is required:</p> <ul style="list-style-type: none">• Illumina paired-end/high-quality mate-pairs/unpaired reads• IonTorrent paired-end/high-quality mate-pairs/unpaired reads• PacBio CCS reads (at least 5 reads coverage is recommended) <p>It is strongly suggested to provide multiple paired-end and mate-pair libraries according to their insert size (from smallest to longest).</p> <p>Additionally, one may input Oxford Nanopore reads, Sanger reads, contigs generated by other assembler(s), etc. Note that Illumina and IonTorrent libraries should not be assembled together. All other types of input data are compatible.</p> <p>It is also possible to set up reads orientation (forward-reverse (fr), reverse-forward (rf), forward-forward (ff)) and specify whether paired reads are separate or interlaced.</p> <p>Illumina, IonTorrent or PacBio CCS reads should be provided in FASTQ format. Illumina or PacBio read may also be provided in FASTA format. Error correction should be skipped in this case (see the "Running mode" parameter). Sanger, Oxford Nanopore, and PacBio CLR reads can be provided in both formats since SPAdes does not run error correction for these types of data.</p> <p>To configure input data use the following button:</p> <div data-bbox="315 854 1266 1318"></div>	

Configure SPAdes Input Type

Required input (at least one)

Illumina/Ion Torrent reads

Sequencing platform
Illumina

☒ Paired-end reads
fr
Separate reads

☐ High-quality mate-pairs
fr
Separate reads

☐ Unpaired reads

☐ PacBio CCS reads

Additional input

Illumina/Ion Torrent reads

☐ Mate-pairs
fr
Separate reads

☐ PacBio CLR reads
☐ Sanger reads

☐ Oxford Nanopore reads
☐ Trusted contigs

☐ Untrusted contigs

Help
Cancel
OK

Dataset type	Input dataset type.	Multi Cell
Running mode	Running mode.	Error correction and assembly
K-mers	k-mersizes (-k).	auto
Number of threads	Number of threads (-t).	16
Memory limit (Gb)	Memory limit (-m).	250
Output folder	Folder to save Spades output files.	Auto

Parameters in Workflow File

Type: spades-id

Parameter	Parameter in the GUI	Type
output-dir	Output directory	string
dataset-type	Dataset type	string
running-mode	Running mode	string

k-mer	K-mers	<i>numeric</i>
threads	Number of threads	<i>numeric</i>
memlimit	Memory limit (Gb)	<i>numeric</i>

Input/Output Ports

The element has 1 *input port*:

Name in GUI: Spades data

Name in Workflow File: in-data

Slots:

Slot In GUI	Slot in Workflow File	Type
URL of a file with right pair reads	url	<i>string</i>
URL of a file with reads	url	<i>string</i>

And 1 *output port*:

Name in GUI: SPAdes output data

Name in Workflow File: out-data

Slots:

Slot In GUI	Slot in Workflow File	Type
Scaffolds URL	url	<i>string</i>
Contig URL	url	<i>string</i>